

AGCATCCTGA	GTAATGAGTG	GCCTGGGCCG	GAGCAGGCCA	GGTGGCCGGA	GCCGTGTGGA	60
CCAGGAGGAG	CGCTTTCAC	AGGGCCTGTG	GACGGGGGTG	GCTATGAGAT	CCTGCCCCGA	120
AGAGCAGTAC	TGGGATCCTC	TGCTGGGTAC	CTGCATGTCC	TGCAAAACCA	TTTGCAACFA	180
TCAGAGCCAG	CGCACCTGTG	CAGCCTTCTG	CAGGTCACTC	AGCTGCCGCA	AGGAGCAACG	240
CAAGTTCTAT	GACCATCTCC	TGAGGGAGTG	CATCAGCTGT	GCCTCCATCT	GTGGACAGCA	300
CCCTAAGCAA	TGTGCATACT	TCTGTGAGAA	CAAGCTCAGG	AGCCCAAGTA	ACCTTCCACC	360
AGAGCTCAGG	AGACAGCGGA	GTGGAGAAGT	TGAAAACAAT	TCAGACAAC	CGGGAAGGTA	420
CCAAGGATTG	GAGCAGAGAG	GCTCAGAAAG	AAGTCCAGCT	CTCCCGGGGC	TGAAGCTGAG	480
TGCAGATCAG	GTGGCCCTGG	TCTACAGCAC	GCTGGGGCTC	TGCTGTGTG	CCGTCCTCTG	540
CTGCTTCTCTG	GTGGCGGTGG	CCTGCTTCTT	CAAGAAGAGG	GGGATCCCT	GCTCTGCECA	600
GCCCCGCTCA	AGGCCCCGTC	AAAGTCCGGC	CAAGTCTTCC	CAGGATCAAG	CGATGGAAGC	660
CGGCAGCCCT	GTGAGCACAT	CCCCCGAGCC	AGTGAGAGCC	TGCAGCTTCT	GCTTCCCTGA	720
GTGCAAGGCG	CCCACGCAGG	AGAGCGCAGT	CAGCCCTGGG	ACCCCGGACC	CCACTTGTGG	780
TGGAAGGTGG	GGGTGCCACA	CCAGGACCAC	AGTCTGCGAG	CTTGCCAC	ACATCCAGCA	840
CAGTGGCCTT	GGCATTGTGT	GTCTGCCTGC	CCAGGAGGGG	GGCCAGGTG	CATAAATGGG	900
GGTCAGGGAG	GGAAAGGAGG	AGGGAGAGAG	ATGGAGAGGA	GGGAGAGAG	AAAGAGAGGT	960
GGGAGAGGG	GAGAGAGATA	TGAGGAGAGA	GAGACAGAGG	AGGCAGAAAG	GGAGAGAAAC	1020
AGAGGAGACA	GAGAGGGAGA	GAGAGACAGA	GGGAGAGAGA	GACAGAGGGG	AAGAGAGGCA	1080
GAGAGGGAAA	GAGGCAGAGA	AGGAAAGAGA	CAGGCAGAGA	AGGAGAGAGG	CAGAGAGGGA	1140
GAGAGGCAGA	GAGGGAGAGA	GGCAGAGAGA	CAGAGAGGGA	GAGAGGGACA	GAGAGAGATA	1200
GAGCAGGAGG	TCGGGGCACT	CTGAGTCCCA	GTTCCAGTGC	CAGCTGTAGG	TGCTCATCAC	1260
CTAACACAC	GTGCAATAAA	GTCCTCGTGC	CTGCTGCTCA	CAGCCCCGCA	GAGCCCCCTC	1320
TCTTGAGAAA	TAAACCTTT	GGCAGCTGCC	CTTCTCTAAA	AAAAAAAAAA	AAAAAA	1377

FIGURE 1A

Met Ser Gly Leu Gly Arg Ser Arg Arg Gly Gly Arg Ser Arg Val Asp  
 1 5 10 15  
 Gln Glu Glu Arg Phe Pro Gln Gly Leu Trp Thr Gly Val Ala Met Arg  
 20 25 30  
 Ser Cys Pro Glu Glu Gln Tyr Trp Asp Pro Leu Leu Gly Thr Cys Met  
 35 40 45  
 Ser Cys Lys Thr Ile Cys Asn His Gln Ser Gln Arg Thr Cys Ala Ala  
 50 55 60  
 Phe Cys Arg Ser Leu Ser Cys Arg Lys Glu Gln Gly Lys Phe Tyr Asp  
 65 70 75 80  
 His Leu Leu Arg Asp Cys Ile Ser Cys Ala Ser Ile Cys Gly Gln His  
 85 90 95  
 Pro Lys Gln Cys Ala Tyr Phe Cys Glu Asn Lys Leu Arg Ser Pro Val  
 100 105 110  
 Asn Leu Pro Pro Glu Leu Arg Arg Gln Arg Ser Gly Glu Val Glu Asn  
 115 120 125  
 Asn Ser Asp Asn Ser Gly Arg Tyr Gln Gly Leu Glu His Arg Gly Ser  
 130 135 140  
 Glu Ala Ser Pro Ala Leu Pro Gly Leu Lys Leu Ser Ala Asp Gln Val  
 145 150 155 160  
 Ala Leu Val Tyr Ser Thr Leu Gly Leu Cys Leu Cys Ala Val Leu Cys  
 165 170 175  
 Cys Phe Leu Val Ala Val Ala Cys Phe Leu Lys Lys Arg Gly Asp Pro  
 180 185 190  
 Cys Ser Cys Gln Pro Arg Ser Arg Pro Arg Gln Ser Pro Ala Lys Ser  
 195 200 205  
 Ser Gln Asp His Ala Met Glu Ala Gly Ser Pro Val Ser Thr Ser Pro  
 210 215 220  
 Glu Pro Val Glu Thr Cys Ser Phe Cys Phe Pro Glu Cys Arg Ala Pro  
 225 230 235 240  
 Thr Gln Glu Ser Ala Val Thr Pro Gly Thr Pro Asp Pro Thr Cys Ala  
 245 250 255  
 Gly Arg Trp Gly Cys His Thr Arg Thr Thr Val Leu Gln Pro Cys Pro  
 260 265 270  
 His Ile Pro Asp Ser Gly Leu Gly Ile Val Cys Val Pro Ala Gln Glu  
 275 280 285  
 Gly Gly Pro Gly Ala  
 290

FIGURE 1B

(start and stop codons are in bold type)

AGCAAGTTCA	GCCTGGTTAA	GTCCAAGCTG	AATTCCGGTC	AAAGTTCAAG
TAGTGATATG	GATGACTCCA	CAGAAAGGGA	GCAGTCACGC	CTTACTTCTT
GCCTTAAGAA	AAGAGAAGAA	ATGAAACTGA	AGGAGTGTGT	TTCCATCCTC
CCACGGAAGG	AAAGCCCCTC	TGTCCGATCC	TCCAAAGACG	GAAAGCTGCT
GGCTGCAACC	TTGCTGCTGG	CACTGCTGTC	TTGCTGCCTC	ACGGTGGTGT
CTTTCTACCA	GGTGGCCGCC	CTGCAAGGGG	ACCTGGCCAG	CCTCCGGGCA
GAGCTGCAGG	GCCACCACGC	GGAGAAGCTG	CCAGCAGGAG	CAGGAGCCCC
CAAGGCCGGC	CTGGAGGAAG	CTCCAGCTGT	CACCGCGGGA	CTGAAAATCT
TTGAACCACC	AGCTCCAGGA	GAAGGCAACT	CCAGTCAGAA	CAGCAGAAAT
AAGCGTGCCG	TTCAGGGTCC	AGAAGAAACA	GTCACTCAAG	ACTGCTTGCA
ACTGATTGCA	GACAGTGAAA	CACCAACTAT	ACAAAAAGGA	TCTTACACAT
TTGTTCCATG	GCTTCTCAGC	TTTAAAAGGG	GAAGTGCCCT	AGAAGAAAAA
GAGAATAAAA	TATTGGTCAA	AGAAACTGGT	TACTTTTTTA	TATATGGTCA
GGTTTTATAT	ACTGATAAGA	CCTACGCCAT	GGGACATCTA	ATTCAGAGGA
AGAAGGTCCA	TGTCTTTGGG	GATGAATTGA	GTCTGGTGAC	TTTGTTCGA
TGTATTCAAA	ATATGCCTGA	AACACTACCC	AATAATTCTT	GCTATTCAGC
TGGCATTGCA	AAACTGGAAG	AAGGAGATGA	ACTCCAACCT	GCAATACCAA
GAGAAAATGC	ACAAATATCA	CTGGATGGAG	ATGTCACATT	TTTTGGTGCA
TTGAAACTGC	TGTGACCTAC	TTACACCATG	TCTGTAGCTA	TTTTCTCTCC
TTTCTCTGTA	CCTCTAAGAA	GAAAGAACT	AACGTGAAAT	ACCAAAAAAA
AAAAAAAAAA	AAAAAGATCT	TTAATTAAGC	GGCCGCAAGC	TTATTCCCTT
TAGTGAG				

FIGURE 2A

Translation in relevant reading frame (3' 5'):

MDDSTEREQS	RLTSCCLKRE	EMKLKECVSI	LPRKESPSVR	SSKDGKLLAA
TLLLALLSCC	LTVVSFYQVA	ALQGDLASLR	AELQGHHAEK	LPAGAGAPKA
GLEEAPAVTA	GLKIFEPPAP	EGNSSQNSR	NKRAVQGPEE	TVTQDCLQLI
ADSETPTIQK	GSYTFVPWLL	SFKRGSAL EE	KENKILVKET	GYFFIYGQVL
YTDKTYAMGH	LIQRKKVHVF	GDELSLVTLF	RCIQNMPETL	PNNSCYSAGI
AKLEEGDELQ	LAIPRENAQI	SLDGDVTFFG	ALKLL	

FIGURE 2B

Translation in relevant reading frame (3' 5'):

MARRLWILSL LAVTLTVALA APSOKSKRRT SSDRMKQIED KIEEILSKIY  
HIENEIARIK KLIGERTRSG NSSQNSRNKR AVQGPEETVT QDCLQLIADS  
ETPTIQKGSY TFVPWLLSFK RGSALEEKEN KILVKETGYF FIYGQVLYTD  
KTYAMGHLIQ RKKVHVFGDE LSLVTLFRCI QNMPETLPNN SCYSAGIAKL  
EEGDELQLAI PRENAQISLD GDVTFFGALK LL  
(SEQ ID NO:3)

FIGURE 3

1,2-di-~~4,4'-diiodo-2,2'-bipyridine~~  
Plate Binding assay-NLLZ + HuTACIFC (Goat anti-human Fc) 1/6/99  
25-FEB-99

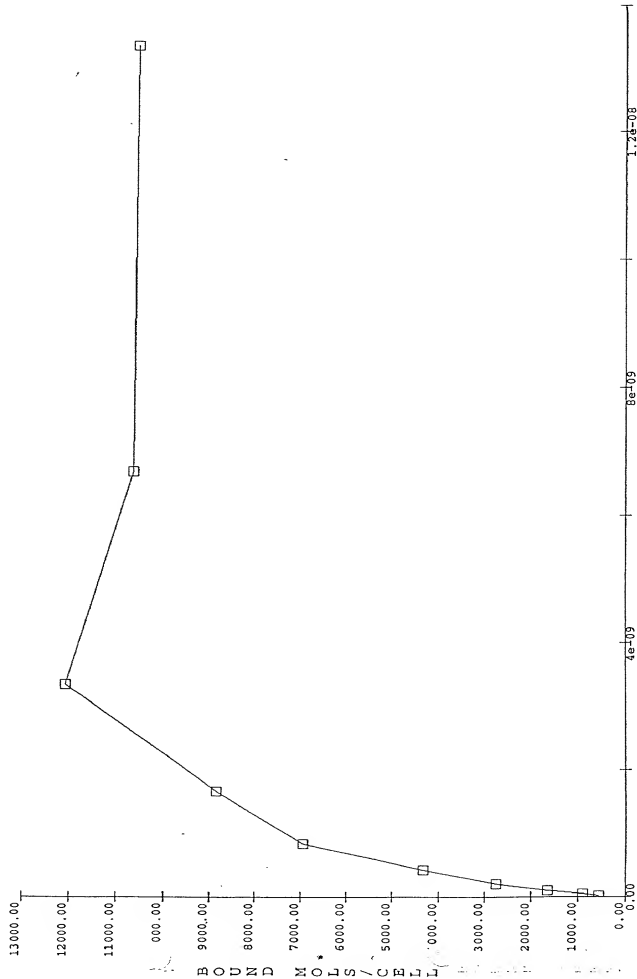


FIGURE 4A

1:2 d.h.

Plate Binding assay-NLIZ + HUPACTPC (Goat anti-Human Fc) 1/5/99  
25-FEB-99

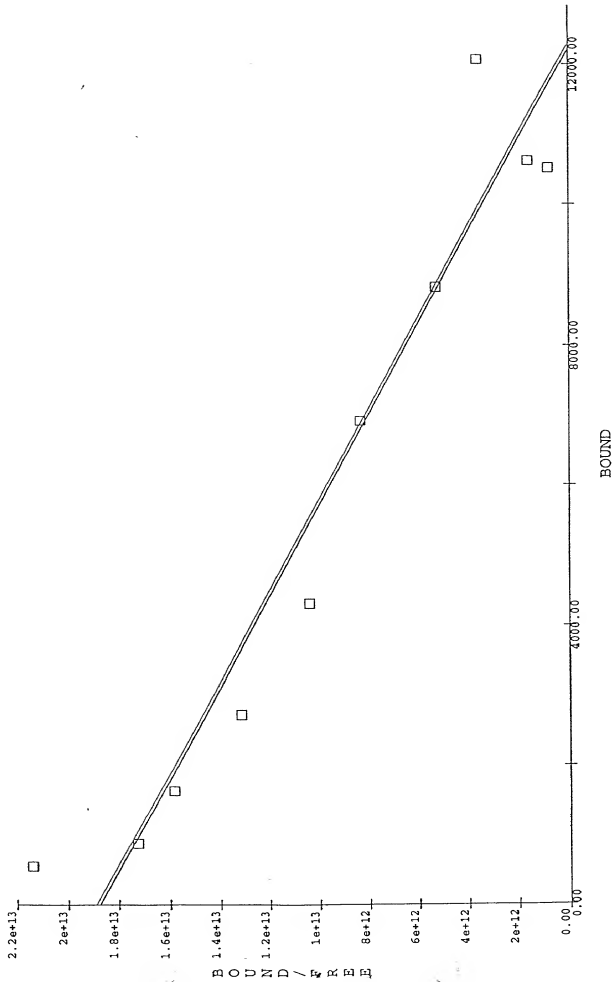
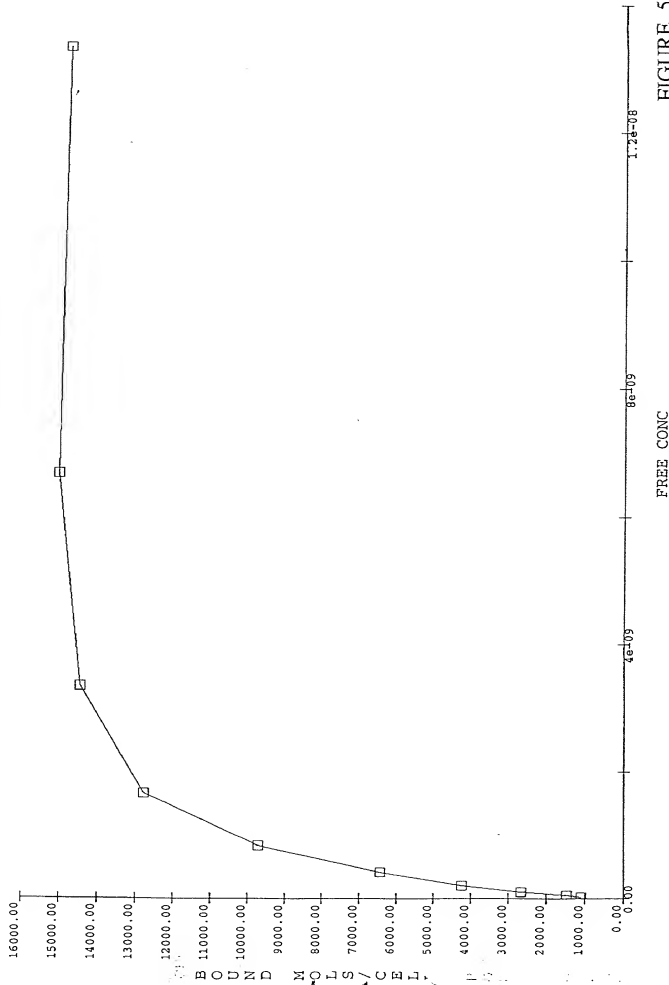


FIGURE 4B

1:54:11 PM 1999 FEB 25

Plate Binding assay-NLLZ + HuTAC1PC (Goat anti-hu Fc) 1/6/99 duplicate

25-FEB-99



FREE CONC

FIGURE 5A



1/5/99 10:55:58  
 Plate Binding assay-NLIZ + HuAcIFC (Goat anti-hu Fc) 1/6/99 duplicate  
 25-FEB-99

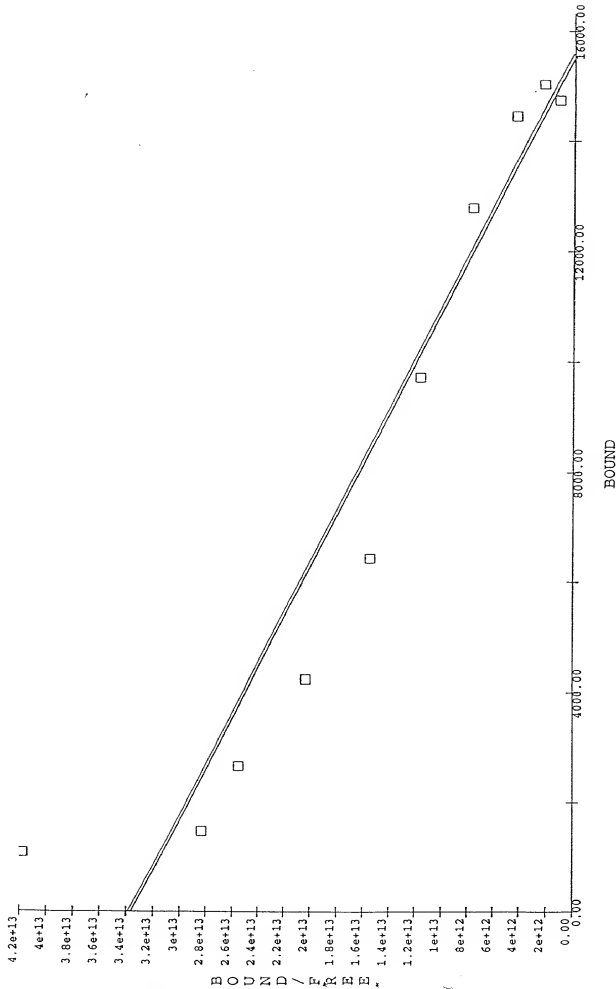
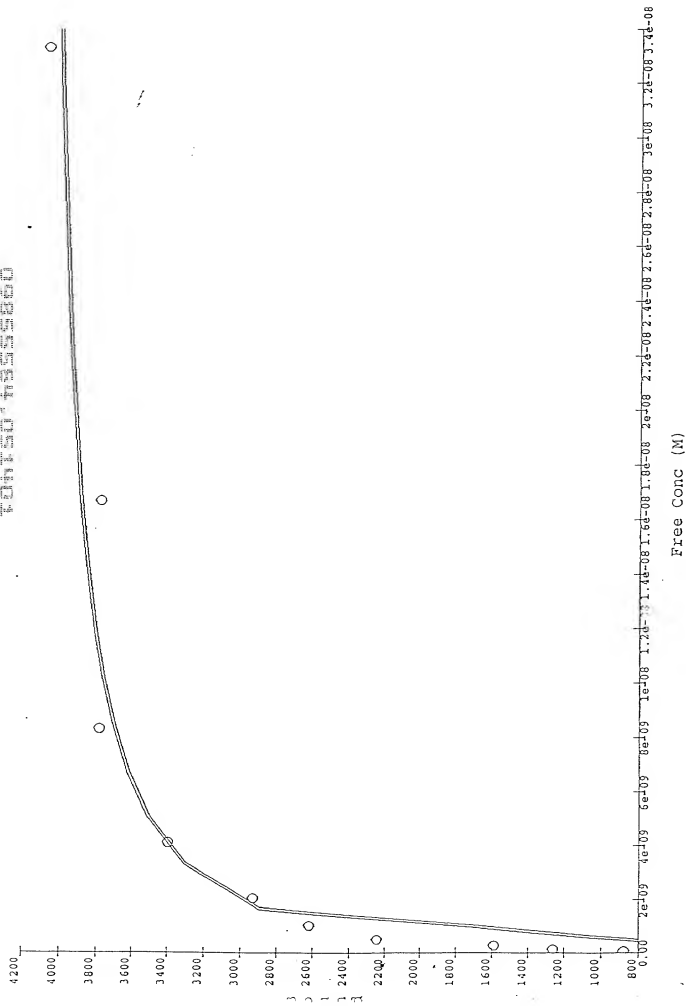


FIGURE 5B

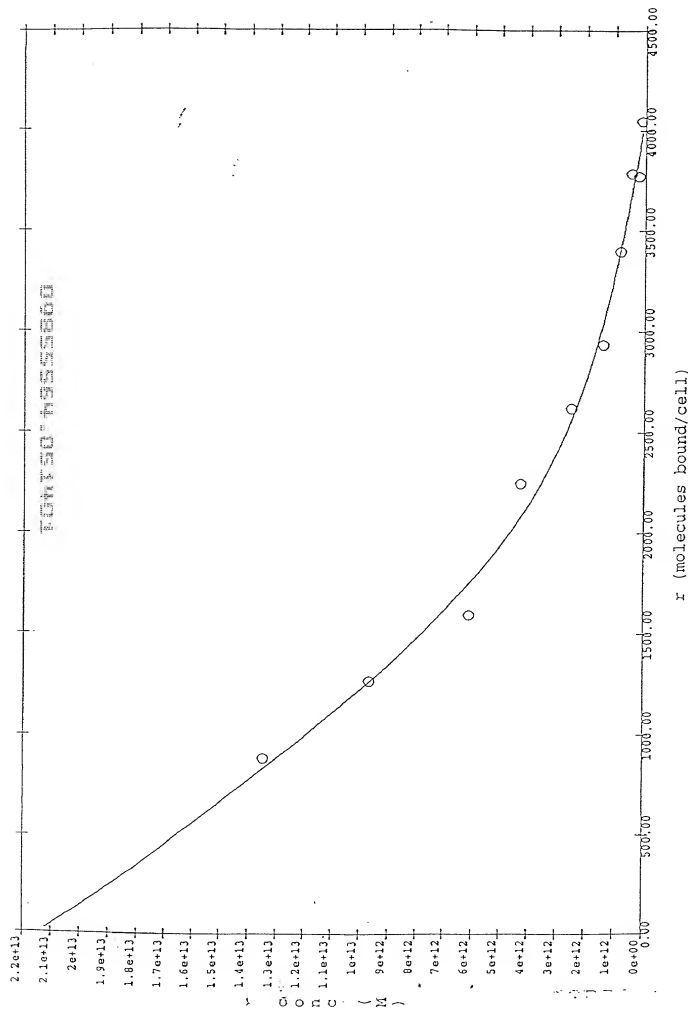
FORWARD 43555860



○ Data points

$$\frac{(2.1e+03 * 5.7e+08 * X) / (1 + 5.7e+08 * X) + (1.9e+03 * 1.0e+10 * X) / (1 + 1.0e+10 * X)}{\text{Free Conc (M)}}$$

FIGURE 6A



r (molecules bound/cell)

○ Data points

—  $(2.1e+03 \cdot 5.7e+08 \cdot x) / (1+5.7e+08 \cdot x) + (1.9e+03 \cdot 1.0e+10 \cdot x) / (1+1.0e+10 \cdot x)$

FIGURE 6B